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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2518.26 Seconds

(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-8

Perfect score: 1017
Sequence: 1 atgaagtcacccgtgtctat.....caggtcgcaagaagtaa 1017Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank1:
1: gb ba:*
2: gb htg:*
3: gb in:*
4: gb ov:*
5: gb om:*
6: gb pat:*
7: gb ph:*
8: gb pl:*
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13: gb un:*
14: gb vi:*
15: em ba:*
16: em fun:*
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18: em in:*
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21: em or:*
22: em ov:*
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38: em sy:*
39: em htgo hum:*
40: em htgo mus:*
41: em htgo other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251.6	24.7	840	3	AB045172
2	246.8	24.3	828	3	AB045179
3	246.2	24.0	780	3	AB045168
4	241.8	23.8	808	3	AB045178
5	240.6	23.7	710	3	AB045171
6	233.4	22.9	774	3	AB045170
7	232.8	22.9	781	3	AB045165
8	231	22.7	784	3	AB045167
9	227.8	22.4	798	3	AB045166
10	221.4	21.8	1443	8	FSOKCH
11	221.4	21.8	1473	6	A21795
12	221.4	21.8	1473	6	A23637
13	221.4	21.8	1473	6	A23646
14	221.4	21.8	1473	6	A23955
15	221.4	21.8	1473	6	A23959
16	221.4	21.8	1473	6	A41660
17	221.4	21.8	1473	6	AR072922
18	221.4	21.8	1473	6	BD002249
19	221.4	21.8	1473	6	BD010853
20	221.4	21.8	1473	6	113885
21	221.4	21.8	1473	6	121317
22	221.4	21.8	1473	6	157984
23	217.4	21.4	761	3	AB045175
24	213.6	21.0	785	3	AB045169
25	212.2	20.9	759	3	AB045174
26	212.2	20.9	802	3	AB045176
27	211.8	20.8	783	3	AB045173
28	210.6	20.7	785	3	AB045177
29	207.4	20.4	1423	6	AR094309
30	204	20.1	912	6	A68076
31	204	20.1	912	6	AR163170
32	202.8	19.9	919	6	A68072
33	202.8	19.9	919	6	AR163168
34	200.6	19.7	924	6	A68074
35	200.6	19.7	924	6	AR163169
36	188	18.5	922	6	A68078
37	188	18.5	922	6	AR163171
38	186.8	18.4	922	6	A68070
39	186.8	18.4	922	6	AR163167
40	186	18.3	1154	6	AR094308
41	184	18.1	1174	6	A92311
42	184	18.1	1174	6	AR075389
43	184	18.1	1174	6	AR094310
44	179.4	17.6	1057	6	BD002248
45	179.4	17.6	1060	6	A21793

ALIGNMENTS

RESULT 1
LOCUS AB045172 840 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
ACCESSION AB045172
VERSION AB045172.1 GI:8926976
KEYWORDS Reticulitermes speratus hindgut symbiont 130484
SOURCE Clon:8-44.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE 1 (sites)
AUTHORS Ohnoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
 21020023
 2 (bases 1 to 840)
 Ohkuma, M.
 Direct Submission
 Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory, Hirotsawa

BASE COUNT	227 a	157 c	.200 g	256 c
ORIGIN				

Query Match	24.7%;	Score 251.6;	DB 3;	Length 870;
Best Local Similarity	65.4%;	Pred. No. 1.2e-56;		
Matches 403; Conservative	0;	Mismatches 204;	Indels 9;	Gaps 2

[illegible]

QY	1002	TTGCGAAGGAAGTAA	1017
Db	675	TTGCAAGCGAAGTTAA	690

RESULT 2	
AB045179	828 bp mRNA linear INV 14-FEB-2001
LOCUS	Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION	cellulase homologue, clone:6-47, complete cds.
ACCESSION	AB045179
VERSION	AB045179.1 GI:8926990
KEYWORDS	Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
SOURCE	clone:6-47

FEATURES

Location/Qualifiers

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CDS

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Best Local Similarity	64.9%;	Pred. No. 2.3e-55;		
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408	TGTTTCACAACTCTGTTATTTGGGATTTGTTGAAGCTCTTGACAGCTGCGCTTGAAAACG			467
79	TGGAGGACATCAACGGTATTTGGATTTGTCGAAGCGTCATAGTCAGGAGAAAAAAGC			138
468	TTCTGTCACTGGTCTGTTGAACCTGTGCTCCAACTGATCTCTTTATTAG-----A			521
139	TGCTGTGACTCAGCGCTTGATGATACGTGTGGAAGAAATGGGCAACAAGACTTGCAAGCA			198
522	TGCCAAATGCTCAAAAGTGTGTGAACGGTGTATGTTTCATGTGTAAACAACAACCAAC			581
199	TGACACAGTAAATTCAGAGTTGTATGTGGCAGATGATACATGTGTATATGATCAAGCACC			258
582	TTGGGCTGTCAATGATAGACTCGCTTAAGGTTTCGCTGTGCTGCTCTCTATATTCGTGGCTTCA			641
259	ATGGGCTGTATATACCTCAAGTGTCTATGGTTTTCGCACTGCAAGTTGCTGTGG---AGG			315
642	CGAAGCTGAATGAGTGTGTGCTGTATGAAATTGACCTTCACTTGTGGCGGTGCTTTCGG			701

Db 316 TGAGACTGAGCTTTGTCATTGCTATGAGCTTACGTTACGAGTGGCCAGTAATGG 375
 Qy 702 AAGAAGATGGTTGTTCAAGTTACCAACCGGTTGGATTTAGGCTTAAACAATTGA 761
 Db 376 AAAAAGATGGTTGTTCAAGTTACCAACCGGTTGGATTTAGGCTTAAACAATTGA 435
 Qy 762 TTTCGAATGCCCCGTTGGTGGCTGTGATCTTCAATGGCTGTGCTCAATGGGCGC 821
 Db 436 TCTTGAATTCAGAGAGAGAGTGTGAAATTACAAATGAGTCACTAGCAATGAGTGC 495
 Qy 822 TCCCAATGATGCTGGGAGCTAGATATGTTGTTGCTGCTGTCTGCTGATGCTGC 881
 Db 496 ACTGCTGATGATGGGGAACCGTTATGTTGTTGCTGCTGCTGCTGCTGCTGCTG 555
 Qy 882 TCTTCCCTGCTGCTTCAAGTGTGTTGAATGAGATTCACCTGTTCAAGAACTGCA 941
 Db 556 ACTTCTTCTGCTGCTTCAAGTGTGTTGAATGAGATTCACCTGTTCAAGAACTGCA 615
 Qy 942 TAACCTTACCAATGCTTCAAGAGTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1001
 Db 616 CAACCTTCAATGCTTCAAGAGTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
 Qy 1002 TTGCGAAAGAAAGTAA 1017
 Db 676 TTGCAACGTAATTAA 691
 RESULT 3
 AB045168 780 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:4-44, complete cds.
 ACCESSION AB045168
 VERSION AB045168.1 GI:8926986
 KEYWORDS
 SOURCE
 ORGANISM
 Reticulitermes speratus hindgut symbiont 130484
 Unclassified.
 REFERENCE
 1 (sites)
 Ohnoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family
 45 from the symbiotic protists in the hindgut of the termite
 Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL
 MEDLINE
 21020023
 2 (bases 1 to 780)
 Ohkuma, M.
 Direct Submission
 TITLE Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory, Hiroshima
 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
 Fax:66-48-462-4672)
 FEATURES
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 Location/Qualifiers
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 BASE COUNT
 ORIGIN 196 a 155 c 206 g 223 t
 Query Match 24.0%; Score 244.2; DB 3; Length 780;
 Best Local Similarity 64.4%; Pred. No. 1.1e-54;

Matches 401; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
 Qy 400 TCTGGAGTGGTTCCAACTCGTATTGTTGTTGAAGCTTCTTGAGCTGAGCT 459
 Db 64 TGTACAGTGGCAAAAGACCCGCTATGAGTGTGCTGCAAAAGCTCTGTGGCGAA 123
 Qy 460 GGAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
 Db 124 GCAAAAGCTGATGTCAGCAAAAGCTGATGATGATGATGATGATGATGATGATG 183
 Qy 520 GATGCCAATGCTC-----AAAGTGTGTAACGTTGTAATGTTTCAATGTGAAC 573
 Db 184 GCAAGCAACATACAGTAATAATCGTTGATGATGATGATGATGATGATGATGATG 243
 Qy 574 AACCAACCTTGGGCTGTCATGATGATGATGATGATGATGATGATGATGATGATG 633
 Db 244 CAACCCCGTGGGCGTCAACGATTCATGATGATGATGATGATGATGATGATGATG 303
 Qy 634 GGTCCAAAGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
 Db 304 GAGGTGAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 Qy 694 GCTTGTGAAAGATGTTGTTCAAGTTACCAACCGGTCGATTTAGCTCTTAC 753
 Db 361 GTTAAATGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 754 CACTTGAATTTGCAATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
 Db 421 CAATTATCTCGCATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Qy 814 TGGGGCCCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 873
 Db 481 TCTGTGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 Qy 874 TGTGCTCTCTTCTCTGCTGCTTCAAGCTGTTGAATGATGATGATGATGATGATG 933
 Db 541 TGTCTCCAGCTTCTCTGCTGCTTCAAGCTGTTGAATGATGATGATGATGATGATG 600
 Qy 934 AACTGTATTAACCTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 993
 Db 601 AATGCCACATTCGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Qy 994 CGCTCAGTTGCGAAAGATTA 1016
 Db 661 AAAACCAATTGCAGACCAATTA 683
 RESULT 4
 AB045178 808 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:45-6, complete cds.
 ACCESSION AB045178
 VERSION AB045178.1 GI:8926988
 KEYWORDS
 SOURCE
 Reticulitermes speratus hindgut symbiont 130484
 Unclassified.
 REFERENCE
 1 (sites)
 Ohnoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family
 45 from the symbiotic protists in the hindgut of the termite
 Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL
 MEDLINE
 21020023
 2 (bases 1 to 808)
 Ohkuma, M.
 Direct Submission
 TITLE Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory, Hiroshima
 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
 Fax:66-48-462-4672)

Fax:66-48-462-4672)

FEATURES

source

Location/Qualifiers
1..808
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130484"
/clone="45-6"
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CDS

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Matches 395; Conservative 0; Mismatches 212; Indels 6; Gaps 2;

OY 408 TGGTTCACAACTCGTTATTGGAGATTGTTAAAGCTTCTTGACGTGGCTCGAAAGC 467
DB 81 TGGCAGAACAACTCGCTATTGGATTGTTAAAGGGAGCTGTGATGGATGCGAAGC 140
OY 468 TTCTGTCACTGTCTCTGTGTGACACCTGCTCCCATGTATCTCTTATTAGATGCCAA 527
DB 141 TTCCGTGTCCAAAGCCCGTGTGACACATGTGCAAAAGATGMAACATCGAGTTGCAACAG 200
OY 528 TGGTCAAAAGGTTG---TAAAGGTGTAAATGTTTATGTTGAAACAACAACCAACCTG 584
DB 201 CGAAATATGAGCTTGTGATAGTGGGCGACACATATGTGTATGATCAAAACCGCG 260
OY 585 GGGTGTCAATGATGAGCTGCTTACGTTGGCTGCTCTATTTGCTGCTCAACGA 644
DB 261 TGGTGTCAATGATTCATATGATGAGTGGTGTGCTGCGGCTGTTCAAGGTGTGA 320
OY 645 AGCTGATGAGTGTGCTGTTATGATTAATGACCTTCACTTGGCGCTGCTTGTGAAA 704
DB 321 AGCGG---CGTGTGTACGTGTATGAACTCACTTCACTTGGCGCTGTTATGAAA 377
OY 705 GAATATGCTGTTCATGATTAACCAACCGGTGCGATTAAGCTTCAACAATTGATTT 764
DB 378 GAATATGATGCTGTTCATGATTAACCAACCGGTGCGATTCCTTCAACAATTGATTT 437
OY 765 GCAATGCGCGGTGAGGCTGTGTATCTTCAATGAGTGTGCTCAATGGGCGGCTCC 824
DB 438 TGGATTTCCGGGCGAGAGGTGTGACCTTCAACGGTGTGACCTTCAATGGGCGAC 497
OY 825 CAATGATGCTGGGAGAGCTAATATGAGTGTGACGCTGTCTCTGACTGTGCTCTCT 884
DB 498 TGCAGATGATGGGAGAGCGCATATGAGGAGTGTCTCTCAAGAGTGTGTTCAAGT 557
OY 885 TCCCTGTGCTTTCAAGCTGTTGTAATGGAATTCATAGTGTCAAGAACTGTATTA 944
DB 558 TCCCTGTGCTTTCAAGCGCGGTGCGCATGTGCTGTTGACTGTTCAAAATGTGTATA 617
OY 945 CCTACCATGACCTTCAAGAGATTAACCTGCTGCTGTAATTAACATCTCGTCAGGTTG 1004
DB 618 TCGGTCAATTAATTAACGAAGATGATGTTCAGAGTGTGACATGACAGAAACCAATTTG 677
OY 1005 CGAAAGAAAGTAA 1017
DB 678 CAGACGCCAGTAA 690

RESULT 5

AB045171

LOCUS AB045171 710 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:7-50, complete cds.

ACCESSION AB045171 GI:8926974
VERSION AB045171.1
KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:7-50.
SOURCE Reticulitermes speratus hindgut symbiont 130484
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE 1. (ites)
Ohno,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2 (bases 1 to 710)
Ohkuma,M.
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory, Hirotsawa
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)

FEATURES

source

Location/Qualifiers
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Query Match 23.7%; Score 240.6; DB 3; Length 710;
Best Local Similarity 64.1%; Pred. No. 1e-53;
Matches 398; Conservative 0; Mismatches 214; Indels 9; Gaps 2;

OY 403 GCGATGCTTCCAACTCGTTATTGGAGATTGTTAAAGCTTCTTGACGTGGCTGGA 462
DB 62 GACAGCGAAGAACACCCGTTATTGGATTGTGCAAGCGAGCTGTGGGAAAAA 121
OY 463 AAGCTTGTCACTGCTCGTTGACACCTGCTCCAAATGATATCTTATTAG-- 520
DB 122 AAGCTGCTGTTCACAGCTGTGTACACTTGTGAAAAATGAGACACAGAGTGG 181
OY 521 ----ATGCCATGCTCAAGAGTGTGTAAAGTGTAAATGTTTCAATGTGTAAACAAC 576
DB 182 AGCAATGACACTGTGAATACAGTGTGTATGTGAGAAAGATATATATATATCA 241
OY 577 CAACCTTGGGCTGTCAATGATGAGCTGCTTACAGTTTGGCTGCTCTTATTTGGC 636
DB 242 GACCATGGGAGATTAATCTGTGTGGTACAGGTTTGTGCTGAGCTGTGTG- 300
OY 637 TCCAAAGAGCTGATGTTGTGGCTGTATGATTAATGACCTTCACTTGGCGGTGT 696
DB 301 --GGGCGAAGCGAGCTGTGTCAATTCATAGCTTCAATTCACAGTGAACAGG 358
OY 697 TCTGAAAAGAGATGTTGTTCAAGTTACACACCGGTGCGATTTAGGCTTAAACAC 756
DB 359 AATGAAAAGAGATGTTGTTCAAGTTACACACCGGTGCGATTTAGGCTTAAACAC 418
OY 757 TTTGATTTGCAATGCCCGGTGTGCGTGTATCTTCAATGAGCTGTGCTCAATGG 816
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Db 479 GGTGACCTGCTGATGATGGGAAGCCGATATGAGGTTCATCCCGAGGAATGC 538
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RESULT 6
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 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:8-38, complete cds.
 ACCESSION AB045170
 VERSION AB045170.1 GI:8926972
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-38.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 REFERENCE 1 (sites)
 AUTHORS Ohkuma,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 774)
 AUTHORS Ohkuma,M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroshima 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES
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 BASE COUNT 179 a 144 c 212 g 239 t
 ORIGIN

Query Match 22.9%; Score 233.4; DB 3; Length 774;
 Best Local Similarity 64.6%; Pred. No. 9,1e-52;
 Matches 383; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

Qy 406 AGTGGTTCACAACTGTTATGATGTTGTAAGCTTCTTGACAGCTGCGCTGGAAGA 465
 Db 100 ACTGGCAACAACACCCGTTATGATGATGTTGTAAGCTTCTTGACAGCTGCGCTGGAAGA 159
 Qy 466 GCTTCTGCACTGCTGCTGTTGACACCTGCTGCTCAATGATGATCTTTATTAG----- 520
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Qy 521 -ATCCAACTGCTCAAGTGGTGTGAACGCTGTGTAATGTTTCATGTATTAACAACCAA 579
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 Db 340 GAGAGCCGTGCTCTGCAAT--TGTTACAGTTAACTTACCTTCTGGCCGCTTAAT 396
 Qy 700 GGAAGAAGATGTTGTGTCAAGTTACCAACACCGGTGGCATTTAGGCTCTAACACTTT 759
 Db 397 GGAAGAAGATGATGTTGT 456
 Qy 760 GATTGCAATGCCCCGGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
 Db 457 GATCTTGCATTCACAGGT 516
 Qy 820 GCTCCCAATGATGCTGCGGAGCTGATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
 Db 517 GCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 576
 Qy 880 TCTCTCCCTGCTGCTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
 Db 577 CAGTTCCGTTGGGACATTCAGAGCTGTGCTGCCAGTGGCTTTTGTGCTGTTCACAAAGC 636
 Qy 940 GATTAACCTTACATGACCTTCAAGGAAGTACCTGCTGCTGTGAATTAAGTAC 992
 Db 637 GATTAACCTTACATGACCTTCAAGGAAGTACCTGCTGCTGTGAATTAAGTAC 689

RESULT 7
 AB045165 781 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:2-54, complete cds.
 ACCESSION AB045165
 VERSION AB045165.1 GI:8926962
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:2-54.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 REFERENCE 1 (sites)
 AUTHORS Ohkuma,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 781)
 AUTHORS Ohkuma,M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroshima 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES
 source location/Qualifiers
 1..781
 /organism="Reticulitermes speratus hindgut symbiont 130484"
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 25..687
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 /db_xref="GI:8926963"
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WGSRYGVSRSECSQLEPSGLDAGCQWRPFQNDPNDPNSINPNVSCPEGLANTNCR
 BASE COUNT 193 a 143 c 210 g 235 t
 ORIGIN

Query Match 22.7%; Score 232.8; DB 3; Length 784;
 Best Local Similarity 63.4%; Pred. No. 1.3e-51;
 Matches 392; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

406 AGTGGTTCACCACTGTTATGAGATTGTTAAAGCTTCTTGACAGCTGCGTGAAGA 465
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 73 AGTGGCAGAACCAACCGGTAAGTGGATGCGCAAGAAAGATTGGGTGGGAAAGCAAG 132
 |||||
 466 GCTTGTGCTACTGGTCTGTTGACACCGTGGCCCAATGATCTCTTTATTAGT----- 520
 |||||
 133 GCTGATGTAAAGCAAGCTTATGATACATGTGCCAAAGATGGCAACAAGAGTTGCAAGT 192
 |||||
 521 -ATGCCAATGCTCAAGAGGTGTGTAAGGGGTGTAATGTTGATGTAACAAACCA 579
 |||||
 193 AACGATACGGTTAAATCCGGCTGTGATGTGGAAAGATACATGTGTTATGATCAACG 252
 |||||
 580 CTTGGGCTGTCAATGATGAGCTGCTTAAGCTTTGCTGCTCTCTATTTGCTGCTCC 639
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 253 CTTGGCTGTCAATGATGATCTTATGCGCATTTGGCTGCGCTATCTCAAGAGCA 312
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 640 AACGAGCTGATGATGATGCTGTTATGATGATGATGATGATGATGATGATGATGAT 699
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 313 GAGAAAGCTG---CTGTGTCGCAAGTGTACCAATGATGATGATGATGATGATGATGAT 369
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 700 GAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
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 370 GAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429
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 760 GATTGCAAAATGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 819
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 430 GATTTGCTATTCAGAGGGGT 489
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 820 GCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 879
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 490 GCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
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 880 TCT 939
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 550 CAGCTTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
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 940 GATTAACCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
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 610 GATTAACCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
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 1000 GATTGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
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 670 AATTGCAAGCTTAATTA 687

RESULT 8.
 LOCUS AB045167 784 bp mRNA linear INV 14-FEB-2001
 DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 AB045167
 ACCESSION AB045167
 VERSION
 KEYWORDS
 SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-16.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 Unclassified.

REFERENCE
 AUTHORS Ohkuma,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023

REFERENCE 2 (bases 1 to 784)
 AUTHORS Ohkuma,M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroasawa 2-1, Wako-shi, Saitama 351-0198, Japan
 E-mail: morikuma@aimlab.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672

FEATURES
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 Location/Qualifiers
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 /organism="Reticulitermes speratus hindgut symbiont 130484"
 /clone="8-16"
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 /protein_id="BA98037.1"
 /db_xref="GI:8926967"
 /translation="MLVFVFLASLVFSGSGKTRRYMDCCKSGCGMEAKADVSKPIDTCARDGTRVASNDYTKSGCDGSGMYQDTPGVNDSYALGFAPAAISGGERAACNCYELRTSGPVNGKMYQYQYNTNGDLSNPDLAPGGGUGTGTCTGASPADG WGSRYGVSRSECSQLEPSGLDAGCQWRPFQNDPNDPNSINPNVSCPEGLANTNCR RN"

BASE COUNT 202 a 153 c 210 g 219 t
 ORIGIN

Query Match 22.7%; Score 231; DB 3; Length 784;
 Best Local Similarity 63.1%; Pred. No. 4e-51;
 Matches 392; Conservative 0; Mismatches 220; Indels 9; Gaps 2;

402 TGACAGTGGTTCACCACTGTTATGAGATTGTTAAAGCTTCTTGACAGCTGCGTGG 461
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 72 TGACAGTGGCAAAACACCGCTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 131
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 462 AAAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520
 |||||
 132 AAAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
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 521 -----ATGCCAATGCTCAAGAGGTGTGTAAGGGGTGTAATGTTGATGTAACAAACCA 575
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 192 AAGCAACGACACGCTGAAAGTGTGTGATGAGCGGGAAGCAATGATGATGATGATGATGATGAT 251
 |||||
 576 CCAACCTTGGGCTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 635
 |||||
 252 AACACCGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
 |||||
 636 CTCGAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
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 312 AAGCGAAAGGCGCA---TGTCGAACGTTACGAATTAAGTTACCTTCACTTCTGCGCTGC 368
 |||||
 696 TTCTGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
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 369 CAATGCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
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 756 CTTGATTTGCAATATGCCGCTGT 815
 |||||
 429 ATTATATCTCCATACCTTGT 488
 |||||
 816 GGGCGCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
 |||||
 489 TGATGCTCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
 |||||
 876 TGCT 935
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 549 CTCGACATCTCTTCAAGTCTTCAAGCTGCTGCGAGTGGAGATTTGATGATGATGATGATGATGAT 608
 |||||
 936 CTCGATATACCTTCAAGTCTTCAAGCTGCTGCGAGTGGAGATTTGATGATGATGATGATGATGAT 995
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 609 TGCCGACATCTCTCAAGTCTTCAAGCTGCTGCGAGTGGAGATTTGATGATGATGATGATGATGAT 668
 |||||
 996 CTCGATGCGAAAGAAAGTA 1016
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 669 AACCAATTGCAAGCAGCAATTA 689

LOCUS	AB045166	798 bp	mRNA	linear	INV 14-FEB-2001
DEFINITION	Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45				
ACCESSION	AB045166				
VERSION	AB045166.1 GI:8926964				
KEYWORDS	Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,				
ORGANISM	clone:2-6				
REFERENCE	Reticulitermes speratus hindgut symbiont 130484				
AUTHORS	Unclassified.				
TITLE	1 (Rites)				
JOURNAL	Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.				
MEDLINE	Diverse genes of cellulase homologues of glycosyl hydrolase family				
REFERENCE	45 from the symbiotic protists in the hindgut of the termite				
AUTHORS	Reticulitermes speratus				
TITLE	Extremophiles 4 (6), 343-349 (2000)				
JOURNAL	21020023				
MEDLINE	2 (bases 1 to 798)				
REFERENCE	Ohkuma, M.				
AUTHORS	Direct Submission				
TITLE	Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of				
JOURNAL	Physical and Chemical Research), Microbiology Laboratory, Hiroswawa				
MEDLINE	2-, Wako-shi, Saitama 351-0198, Japan				
REFERENCE	(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,				
AUTHORS	Fax:66-48-462-4672)				
TITLE	Location/Qualifiers				
JOURNAL	1. 798				
MEDLINE	/organism="Reticulitermes speratus hindgut symbiont				
REFERENCE	130484"				
AUTHORS	/clone="2-6"				
TITLE	30. .692				
JOURNAL	/codon_start=1				
MEDLINE	/product="family 45 cellulase homologue"				
REFERENCE	/protein_id="BA09036.1"				
AUTHORS	/db_xref="GI:8926965"				
TITLE	/translation="MLVFVFSLSLAVLFGDSKTRRYDCKSGCEAKADVSKPIL				
JOURNAL	TCADGTTGTVASNDTPKSGCDGSDGYMDYDTPGVNDVSLAFMAAIISGEKAA				
MEDLINE	NCAYELTFTSGVNGKMTVQVNTNIGDYMQLFDLAIIGGVGAIINGCTAAGAPAD				
REFERENCE	WGSRRGVSVSRSECSQSLPSGLAQAGQMFQMFQVNDPSNMFNVVSCSELIATNCR				
AUTHORS	RN"				
TITLE	BASE COUNT 195 a 154 c 226 g 222 t 1 others				
JOURNAL	ORIGIN				
MEDLINE	Query Match 22.4%; Score 227.8; DB 3; Length 798;				
REFERENCE	Best Local Similarity 62.8%; Pred. No. 2.9e-50;				
AUTHORS	Matches 390; Conservative 0; Mismatches 222; Indels 9; Gaps 2				
TITLE	402 TGGCAGTGTTCACACACTCGTTATTTGGATTTGTAAAGCTTTGCACTGGCGTGG 461				
JOURNAL	74 TGACAGTGTGCAAAACACAAAGGTATTTGGAGACTGTGCAAGGCGAGTGTGGCTGGAAAGC 133				
MEDLINE	462 AAAAGCTTCTGTCACTGTGCTCGTGTGACACCGTGTCCCAATGGTATCTCTTTATTAAG- 520				
REFERENCE	134 GAAAGCGGACGTGACAGCCCATTTGACATGCGCGGAAAGACGAGACCAACAGATTGC 193				
AUTHORS	521 -----ATGCCAATGTCTCAAAGTGTGTGAACGSGTGTATAGTTTCATGTGTAAACAAG 575				
TITLE	194 GAGCAACGACACCGTGAAGAGGTGTGTGATGTCGGGACGSGTATATGTGTATGATGATCA 253				
JOURNAL	576 CCAACCTGGGCTGTCAATGATGAGACTGGCTTAACGTTTCGCTGCTCTATATTGCTGG 635				
MEDLINE	254 AACACCGTGGGGCGTCAACGACTACATACAGCCCTGTGGCTTGTCTGTGACGACAAATTTACAG 313				
REFERENCE	636 CTCACCAAGAGCTGATGATGTGTGGCTGTATTGAATTTGACCTTCATTTGCGCGCTGC 695				
AUTHORS	314 CGGCGAAGAGGCT---CTTGCTGCAACGTATTATGATTTGACATTCATTGCGCCCGT 370				
TITLE	636 TTTCGAAAGAAAGATGTGTTTCAAGTTACCAACACCGTGGCGATTAAAGCTTTAACA 755				

Db	371	TAAATGGCAAGAAATGACAGTACAGTTTACCAACACTGAGAGCGCACTTGGGTTCCAAATCA	430
Qy	756	CTTGTGATTTGCAATATGCCCGGTGTGCGCTTTGTGATCTTCAAATGGCTGTGTGCTCAATG	815
Db	431	ATTTTATCTTTCGCAATTCACAGCGCGCGGTGTGGGATCTTACAAATGAAATGCAAGGCTCAGTC	490
Qy	816	GGGGCGCTCCCAATATATGATGGCTGGGAGAGCTAGATATATGTGTGTGTCAGCTCTGTCTGACTG	875
Db	491	TGGCGCTCTCTGCTACTACGAGATGGGATGTAGTCGATATGTGTGTGAGATTTCTCTCCGACGGAATG	550
Qy	876	TGCCTCTCTTCCCTCTCTCTCTCTTCAAGCTGTGTTGTAAATGAGATTCAACTGGTTCAAGAA	935
Db	551	CTGGCAACTTCTCTCAGGCTCTTTCAGGCTGCGGTGCGACGTAGGAGATTGATTTGTTGTTCCAAA	610
Qy	936	CTCTGATTAACCTTACCAATGACCTTCAAGAAATTTAACTCTGTCTCTGTAATTAATACTCTG	995
Db	611	CGCCGACAATCCGTCACATGATTTTCAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	670
Qy	996	CTCAGCTTTCGCAAGAAAGTA	1016
Db	671	AACCAATTCGACGCAATTA	691
RESULT 10			
LOCUS	FSOCKH	1443 bp	mRNA linear PLN 28-APR-1995
DEFINITION	Fusarium oxysporum K-family cellulase homologue	complete cds	
ACCESSION	L29381		
VERSION	L29381.1	GI:520822	
KEYWORDS	K-family cellulase homologue; cellulase; homologue.		
SOURCE	Fusarium oxysporum	CDNA to mRNA.	
ORGANISM	Fusarium oxysporum		
REFERENCE	1 (bases 1 to 1443)		
AUTHORS	Shepherd, P.O., Grant, F.J., Oort, P.J., Sprecher, C.A., Foester, D.C.,		
TITLE	Hagen, F.S., Ushnall, A., McKnight, G.L., and O'Hara, P.J.		
JOURNAL	The use of conserved cellulase family-specific sequences to clone		
MEDLINE	cellulase homologue cDNAs from Fusarium oxysporum		
PUBMED	Gene 150 (1), 163-167 (1994)		
FEATURES	95047531		
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	SWCACVALPTTTPVPGKMKI VQSTVTGDLGNHFDLMMGGGVGI FDCSTSEFG		
	ALGAGVYGGISRSRECDSPYELIKDQGWREDEBNNDNPTTEVOVQCPVALLDIS		
	CKRDDSPFAFKGDTASAKRQPSSSAKRTTSAALAAPOPKTKDSPAIVVQKSTPA		
	QPEETKPADKPDNDPVATKTPAATKPAQPVNKKPTTKQVRETKTRGSPATIDATAK		
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BASE COUNT	325 a	448 c	332 g 338 t
ORIGIN			
Query Match	21.8%;	Score 221.4;	DB 8; Length 1443;
Best Local Similarity	63.9%;	Pred. No. 1.7e-48;	
Matches	371;	Conservative	0; Mismatches 201; Indels 9; Gaps 2;
Qy	400	TCGTGACAGTGTCCCAACTCGTTATTGGAGATTGTGTAAAGCTTCTTGACAGCTGCGCT	459
Db	137	TCTGAGAGCGGTCACTACTGATCTGATATCGGAGATGTGTCAGACCTTCTTGCTTGAGAC	196
Qy	460	GGAAGGTTTGTTCACGTGTCTGTGTGACACCTGTGTGCTCCAAATGATGATCTTTATTA	519

BASE COUNT 343 a 453 c 337 g 340 t

ORIGIN

Query Match 21.8%; Score 221.4; DB 6; Length 1473;
 Best Local Similarity 63.9%; Pred. No. 1.7e-48;
 Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

400 TCTGGCAGTGGTTCACAACTCGTTATTTGGATTTGTTAAAGCTTCCTGACGTGCCT 459
 Db TCTGGACGGTCTCACTCTACTGATCTGGAGATTGCTGCAAGCTTCTTCTGCTTGGAGC 210
 151 TCTGGAAAGCGTCACTCTACTGATCTGGAGATTGCTGCAAGCTTCTTCTGCTTGGAGC 210
 460 GGAAGAGCTTCTGCTACTGCTGCTGCTGCACTGCTGCTCAATGCTATCTTTATTA 519
 Db GGAAGAGCTGCTGCTCAAGCGCCCTGCTTAACTGTTGTAAGAAAGCAAGCCCATTTCC 270
 211 GGAAGAGCTGCTGCTCAAGCGCCCTGCTTAACTGTTGTAAGAAAGCAAGCCCATTTCC 270
 520 GATGCCAATGCTCAAAAGTGTGTTAA---CGGTGTAATGTTTCATGTGTAACAACAC 576
 Db GATGCCAATGCTCAAAAGTGTGTTAA---CGGTGTAATGTTTCATGTGTAACAACAC 576
 271 AACACCAATGCTGCAACAGGTTTGAGAGGTGTTCTGCTTATGCTTGCAACCACTAC 330
 577 CAACCTTGGGCTGCTCAATGATGAGCTGCTTACGGTTTGGCTGCTGCTTATTTGCTG 636
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 331 TCTCCCTGGGCTGCTCAACGATGAGCTTGCCTACGGTTTGGCTGCTGCTTACCAATCTCC 390
 637 TCCACGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
 Db GGTCTCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 450
 391 GGTCTCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 450
 697 TCTGGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
 Db AACGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
 451 AAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
 757 TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 816
 Db TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 816
 511 TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 570
 817 GGCCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 876
 Db GGCCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 876
 571 GG-----CAAGGCTCTGCGGCGGTGCCAGTACGGCGGTATCTCTCCGGAAGGAATGT 624
 877 GGCCT 936
 Db GGCCT 936
 625 GATAGCTACCCCGAGCTTCTCAAGGACCGTTGCCACTGCGCATTCGACTGTTGAGAAC 684
 937 TCTGATAACCTTACCATGACCTTCAAGGAAGTAACTGCTTC 977
 Db GCGGACCAACCTTGAACCTTGAAGGAGTCAAGTCC 725

RESULT 13

A23646 1473 bp mRNA linear PAT 23-FEB-1995
 LOCUS F. oxysporum endoglucanase gene.
 DEFINITION A23646
 ACCESSION A23646.1 GI:832892
 VERSION
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 AUTHORS Conventi, A.C., Busch, A. and Baek, A.C.
 TITLE Detergent compositions with high activity cellulase and quaternary
 ammonium compounds
 JOURNAL Patent: EP 0495554-A 3 22-JUL-1992;
 THE PROCTER & GAMBLE COMPANY
 FEATURES location/Qualifiers
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 /organism="Fusarium oxysporum"
 /strain="DSM 2672"
 /db_xref="taxon:5507"
 97..1227
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BASE COUNT 343 a 453 c 337 g 340 t

ORIGIN

Query Match 21.8%; Score 221.4; DB 6; Length 1473;
 Best Local Similarity 63.9%; Pred. No. 1.7e-48;
 Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

400 TCTGGCAGTGGTTCACAACTCGTTATTTGGATTTGTTAAAGCTTCCTGACGTGCCT 459
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 151 TCTGGAAAGCGTCACTCTACTGATCTGGAGATTGCTGCAAGCTTCTTCTGCTTGGAGC 210
 460 GGAAGAGCTTCTGCTACTGCTGCTGCTGCACTGCTGCTCAATGCTATCTTTATTA 519
 Db GGAAGAGCTGCTGCTCAAGCGCCCTGCTTAACTGTTGTAAGAAAGCAAGCCCATTTCC 270
 211 GGAAGAGCTGCTGCTCAAGCGCCCTGCTTAACTGTTGTAAGAAAGCAAGCCCATTTCC 270
 520 GATGCCAATGCTCAAAAGTGTGTTAA---CGGTGTAATGTTTCATGTGTAACAACAC 576
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 Db TCTCCCTGGGCTGCTCAACGATGAGCTTGCCTACGGTTTGGCTGCTGCTTACCAATCTCC 390
 331 TCTCCCTGGGCTGCTCAACGATGAGCTTGCCTACGGTTTGGCTGCTGCTTACCAATCTCC 390
 637 TCCACGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
 Db GGTCTCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 450
 391 GGTCTCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 450
 697 TCTGGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
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 451 AAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
 757 TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 816
 Db TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 816
 511 TTGATTTGCAAAATGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 570
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 Db GGCCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 876
 571 GG-----CAAGGCTCTGCGGCGGTGCCAGTACGGCGGTATCTCTCCGGAAGGAATGT 624
 877 GGCCT 936
 Db GGCCT 936
 625 GATAGCTACCCCGAGCTTCTCAAGGACCGTTGCCACTGCGCATTCGACTGTTGAGAAC 684
 937 TCTGATAACCTTACCATGACCTTCAAGGAAGTAACTGCTTC 977
 Db GCGGACCAACCTTGAACCTTGAAGGAGTCAAGTCC 725

RESULT 14

A23955 1473 bp DNA linear PAT 01-MAR-1995
 LOCUS Endoglucanase gene.
 DEFINITION A23955
 ACCESSION A23955.1 GI:832896
 VERSION
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 AUTHORS Baek, A.C., Busch, A. and Ceulemans, R.A.A.
 TITLE Compact detergent compositions with high activity cellulase

JOURNAL Patient: EP 0495257-A 3 22-JUN-1992;

THE PROCTER & GAMBLE COMPANY

Location/Qualifiers

FEATURES

1..1473

/organism="Fusarium oxysporum"

/db_xref="taxon:5507"

97..1227

/codon_start=1

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SMCCACVYALFTTTPGVKSKMIVOSTNTGDLGNHFDLMPGGVGIPTDCTSEPK

ALGGAOYGGISRSRSCDSYBELDKDCHMRFDWBNADNPTEPOVQCPALDISG

CKRDDSSPPAFKVDTSASKPQSSSAKTTSAALAAOPKTKDSAPVQKSTRPAA

OPEPTKPAKPTQDKPVATKPAATKPVOPVKNPKTKTKVRSKTRGSCPAKTDATARA

SVTPAYVOCGSGSKSAVPNGNLACATGSKCVKNEYYSOCVFN"

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SOURCE

ORGANISM

Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

complex.

REFERENCE

1 (bases 1 to 1473)

McCorquodale, F. and Buech, A.

Dye transfer inhibiting compositions

Patent: EP 0540784-A 3 12-MAY-1993;

JOURNAL

THE PROCTER & GAMBLE COMPANY

Location/Qualifiers

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